

0570
1108

OIPE

#2

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/978,385

DATE: 11/01/2001
 TIME: 13:58:48

Input Set : A:\99-24C1.SEQ.txt
 Output Set: N:\CRF3\11012001\I978385.raw

P5

4 <110> APPLICANT: Piddington, Christopher S.
 5 Petrie, Charles
 6 Shoemaker, Kimberly E.
 7 Bishop, Paul D.
 9 <120> TITLE OF INVENTION: ZACE2: A HUMAN METALLOENZYME
 11 <130> FILE REFERENCE: 99-24C1
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/978,385
 C--> 13 <141> CURRENT FILING DATE: 2001-10-16
 13 <150> PRIOR APPLICATION NUMBER: 60/133,952
 14 <151> PRIOR FILING DATE: 1999-05-13
 16 <150> PRIOR APPLICATION NUMBER: 60/151,181
 17 <151> PRIOR FILING DATE: 1999-08-27
 19 <150> PRIOR APPLICATION NUMBER: 09/563,516
 20 <151> PRIOR FILING DATE: 2000-05-03
 22 <160> NUMBER OF SEQ ID NOS: 11
 24 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 26 <210> SEQ ID NO: 1
 27 <211> LENGTH: 3334
 28 <212> TYPE: DNA
 29 <213> ORGANISM: Homo sapiens
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (35)...(2449)
 35 <400> SEQUENCE: 1
 36 attcagtggga tgtgatcttg gctcacaggg gacg atg tca agc tct tcc tgg ctc 55
 37 Met Ser Ser Ser Ser Trp Leu
 38 1 5
 40 ctt ctc agc ctt gtt gct gta act gct gct cag tcc acc att gag gaa 103
 41 Leu Leu Ser Leu Val Ala Val Thr Ala Ala Gln Ser Thr Ile Glu Glu
 42 10 15 20
 44 cag gcc aag aca ttt ttg gac aag ttt aac cac gaa gcc gaa gac ctg 151
 45 Gln Ala Lys Thr Phe Leu Asp Lys Phe Asn His Glu Ala Glu Asp Leu
 46 25 30 35
 48 ttc tat caa agt tca ctt gct tct tgg aat tat aac acc aat att act 199
 49 Phe Tyr Gln Ser Ser Leu Ala Ser Trp Asn Tyr Asn Thr Asn Ile Thr
 50 40 45 50 55
 52 gaa gag aat gtc caa aac atg aat aat gct ggg gac aaa tgg tct gcc 247
 53 Glu Glu Asn Val Gln Asn Met Asn Asn Ala Gly Asp Lys Trp Ser Ala
 54 60 65 70
 56 ttt tta aag gaa cag tcc aca ctt gcc caa atg tat cca cta caa gaa 295
 57 Phe Leu Lys Glu Gln Ser Thr Leu Ala Gln Met Tyr Pro Leu Gln Glu
 58 75 80 85
 60 att cag aat ctc aca gtc aag ctt cag ctg cag gct ctt cag caa aat 343
 61 Ile Gln Asn Leu Thr Val Lys Leu Gln Leu Gln Ala Leu Gln Gln Asn
 62 90 95 100
 64 ggg tct tca gtg ctc tca gaa gac aag agc aaa cgg ttg aac aca att 391
 65 Gly Ser Ser Val Leu Ser Glu Asp Lys Ser Lys Arg Leu Asn Thr Ile

ENTERED

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| | | | | |
|-----|---|------|-----|--|
| 66 | 105 | 110 | 115 | |
| 68 | cta aat aca atg agc acc atc tac agt act gga aaa gtt tgt aac cca | 439 | | |
| 69 | Leu Asn Thr Met Ser Thr Ile Tyr Ser Thr Gly Lys Val Cys Asn Pro | | | |
| 70 | 120 125 130 135 | | | |
| 72 | gat aat cca caa gaa tgc tta tta ctt gaa cca ggt ttg aat gaa ata | 487 | | |
| 73 | Asp Asn Pro Gln Glu Cys Leu Leu Leu Glu Pro Gly Leu Asn Glu Ile | | | |
| 74 | 140 145 150 | | | |
| 76 | atg gca aac agt tta gac tac aat gag agg ctc tgg gct tgg gaa agc | 535 | | |
| 77 | Met Ala Asn Ser Leu Asp Tyr Asn Glu Arg Leu Trp Ala Trp Glu Ser | | | |
| 78 | 155 160 165 | | | |
| 80 | tgg aga tct gag gtc ggc aag cag ctg agg cca tta tat gaa gag tat | 583 | | |
| 81 | Trp Arg Ser Glu Val Gly Lys Gln Leu Arg Pro Leu Tyr Glu Glu Tyr | | | |
| 82 | 170 175 180 | | | |
| 84 | gtg gtc ttg aaa aat gag atg gca aga gca aat cat tat gag gac tat | 631 | | |
| 85 | Val Val Leu Lys Asn Glu Met Ala Arg Ala Asn His Tyr Glu Asp Tyr | | | |
| 86 | 185 190 195 | | | |
| 88 | ggg gat tat tgg aga gga gac tat gaa gta aat ggg gta gat ggc tat | 679 | | |
| 89 | Gly Asp Tyr Trp Arg Gly Asp Tyr Glu Val Asn Gly Val Asp Gly Tyr | | | |
| 90 | 200 205 210 215 | | | |
| 92 | gac tac agc cgc ggc cag ttg att gaa gat gtg gaa cat acc ttt gaa | 727 | | |
| 93 | Asp Tyr Ser Arg Gly Gln Leu Ile Glu Asp Val Glu His Thr Phe Glu | | | |
| 94 | 220 225 230 | | | |
| 96 | gag att aaa cca tta tat gaa cat ctt cat gcc tat gtg agg gca aag | 775 | | |
| 97 | Glu Ile Lys Pro Leu Tyr Glu His Leu His Ala Tyr Val Arg Ala Lys | | | |
| 98 | 235 240 245 | | | |
| 100 | ttg atg aat gcc tat cct tcc tat atc agt cca att gga tgc ctc cct | 823 | | |
| 101 | Leu Met Asn Ala Tyr Pro Ser Tyr Ile Ser Pro Ile Gly Cys Leu Pro | | | |
| 102 | 250 255 260 | | | |
| 104 | gct cat ttg ctt ggt gat atg tgg ggt aga ttt tgg aca aat ctg tac | 871 | | |
| 105 | Ala His Leu Leu Gly Asp Met Trp Gly Arg Phe Trp Thr Asn Leu Tyr | | | |
| 106 | 265 270 275 | | | |
| 108 | tct ttg aca gtt ccc ttt gga cag aaa cca aac ata gat gtt act gat | 919 | | |
| 109 | Ser Leu Thr Val Pro Phe Gly Gln Lys Pro Asn Ile Asp Val Thr Asp | | | |
| 110 | 280 285 290 295 | | | |
| 112 | gca atg gtg gac cag gcc tgg gat gca cag aga ata ttc aag gag gcc | 967 | | |
| 113 | Ala Met Val Asp Gln Ala Trp Asp Ala Gln Arg Ile Phe Lys Glu Ala | | | |
| 114 | 300 305 310 | | | |
| 116 | gag aag ttc ttt gta tct gtt ggt ctt cct aat atg act caa gga ttc | 1015 | | |
| 117 | Glu Lys Phe Phe Val Ser Val Gly Leu Pro Asn Met Thr Gln Gly Phe | | | |
| 118 | 315 320 325 | | | |
| 120 | tgg gaa aat tcc atg cta acg gac cca gga aat gtt cag aaa gca gtc | 1063 | | |
| 121 | Trp Glu Asn Ser Met Leu Thr Asp Pro Gly Asn Val Gln Lys Ala Val | | | |
| 122 | 330 335 340 | | | |
| 124 | tgc cat ccc aca gct tgg gac ctg ggg aag ggc gac ttc agg atc ctt | 1111 | | |
| 125 | Cys His Pro Thr Ala Trp Asp Leu Gly Lys Gly Asp Phe Arg Ile Leu | | | |
| 126 | 345 350 355 | | | |
| 128 | atg tgc aca aag gtg aca atg gac gac ttc ctg aca gct cat cat gag | 1159 | | |
| 131 | Met Cys Thr Lys Val Thr Met Asp Asp Phe Leu Thr Ala His His Glu | | | |
| 132 | 360 365 370 375 | | | |

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| | | |
|-----|---|------|
| 134 | atg ggg cat atc cag tat gat atg gca tat gct gca caa cct ttt ctg | 1207 |
| 135 | Met Gly His Ile Gln Tyr Asp Met Ala Tyr Ala Ala Gln Pro Phe Leu | |
| 136 | 380 385 390 | |
| 138 | cta aga aat gga gct aat gaa gga ttc cat gaa gct gtt ggg gaa atc | 1255 |
| 139 | Leu Arg Asn Gly Ala Asn Glu Gly Phe His Glu Ala Val Gly Glu Ile | |
| 140 | 395 400 405 | |
| 142 | atg tca ctt tct gca gcc aca cct aag cat tta aaa tcc att ggt ctt | 1303 |
| 143 | Met Ser Leu Ser Ala Ala Thr Pro Lys His Leu Lys Ser Ile Gly Leu | |
| 144 | 410 415 420 | |
| 146 | ctg tca ccc gat ttt caa gaa gac aat gaa aca gaa ata aac ttc ctg | 1351 |
| 147 | Leu Ser Pro Asp Phe Gln Glu Asp Asn Glu Thr Glu Ile Asn Phe Leu | |
| 148 | 425 430 435 | |
| 150 | ctc aaa caa gca ctc acg att gtt ggg act ctg cca ttt act tac atg | 1399 |
| 151 | Leu Lys Gln Ala Leu Thr Ile Val Gly Thr Leu Pro Phe Thr Tyr Met | |
| 152 | 440 445 450 455 | |
| 154 | tta gag aag tgg agg tgg atg gtc ttt aaa ggg gaa att ccc aaa gac | 1447 |
| 155 | Leu Glu Lys Trp Arg Trp Met Val Phe Lys Gly Glu Ile Pro Lys Asp | |
| 156 | 460 465 470 | |
| 158 | cag tgg atg aaa aag tgg tgg gag atg aag cga gag ata gtt ggg gtg | 1495 |
| 159 | Gln Trp Met Lys Lys Trp Trp Glu Met Lys Arg Glu Ile Val Gly Val | |
| 160 | 475 480 485 | |
| 162 | gtg gaa cct gtg ccc cat gat gaa aca tac tgt gac ccc gca tct ctg | 1543 |
| 163 | Val Glu Pro Val Pro His Asp Glu Thr Tyr Cys Asp Pro Ala Ser Leu | |
| 164 | 490 495 500 | |
| 166 | ttc cat gtt tct aat gat tac tca ttc att cga tat tac aca agg acc | 1591 |
| 167 | Phe His Val Ser Asn Asp Tyr Ser Phe Ile Arg Tyr Tyr Thr Arg Thr | |
| 168 | 505 510 515 | |
| 170 | ctt tac caa ttc cag ttt caa gaa gca ctt tgt caa gca gct aaa cat | 1639 |
| 171 | Leu Tyr Gln Phe Gln Phe Gln Glu Ala Leu Cys Gln Ala Ala Lys His | |
| 172 | 520 525 530 535 | |
| 174 | gaa ggc cct ctg cac aaa tgt gac atc tca aac tct aca gaa gct gga | 1687 |
| 175 | Glu Gly Pro Leu His Lys Cys Asp Ile Ser Asn Ser Thr Glu Ala Gly | |
| 176 | 540 545 550 | |
| 178 | cag aaa ctg ttc aat atg ctg agg ctt gga aaa tca gaa ccc tgg acc | 1735 |
| 179 | Gln Lys Leu Phe Asn Met Leu Arg Leu Gly Lys Ser Glu Pro Trp Thr | |
| 180 | 555 560 565 | |
| 182 | cta gca ttg gaa aat gtt gta gga gca aag aac atg aat gta agg cca | 1783 |
| 183 | Leu Ala Leu Glu Asn Val Val Gly Ala Lys Asn Met Asn Val Arg Pro | |
| 184 | 570 575 580 | |
| 186 | ctg ctc aac tac ttt gag ccc tta ttt acc tgg ctg aaa gac cag aac | 1831 |
| 187 | Leu Leu Asn Tyr Phe Glu Pro Leu Phe Thr Trp Leu Lys Asp Gln Asn | |
| 188 | 585 590 595 | |
| 190 | aag aat tct ttt gtg gga tgg agt acc gac tgg agt cca tat gca gac | 1879 |
| 192 | Lys Asn Ser Phe Val Gly Trp Ser Thr Asp Trp Ser Pro Tyr Ala Asp | |
| 193 | 600 605 610 615 | |
| 195 | caa agc atc aaa gtg agg ata agc cta aaa tca gct ctt gga gat aaa | 1927 |
| 196 | Gln Ser Ile Lys Val Arg Ile Ser Leu Lys Ser Ala Leu Gly Asp Lys | |
| 197 | 620 625 630 | |
| 199 | gca tat gaa tgg aac gac aat gaa atg tac ctg ttc cga tca tct gtt | 1975 |

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200  Ala Tyr Glu Trp Asn Asp Asn Glu Met Tyr Leu Phe Arg Ser Ser Val
201                635                640                645
203  gca tat gct atg agg cag tac ttt tta aaa gta aaa aat cag atg att      2023
204  Ala Tyr Ala Met Arg Gln Tyr Phe Leu Lys Val Lys Asn Gln Met Ile
205                650                655                660
207  ctt ttt ggg gag gag gat gtg cga gtg gct aat ttg aaa cca aga atc      2071
208  Leu Phe Gly Glu Glu Asp Val Arg Val Ala Asn Leu Lys Pro Arg Ile
209                665                670                675
211  tcc ttt aat ttc ttt gtc act gca cct aaa aat gtg tct gat atc att      2119
212  Ser Phe Asn Phe Phe Val Thr Ala Pro Lys Asn Val Ser Asp Ile Ile
213  680                685                690                695
215  cct aga act gaa gtt gaa aag gcc atc agg atg tcc cgg agc cgt atc      2167
216  Pro Arg Thr Glu Val Glu Lys Ala Ile Arg Met Ser Arg Ser Arg Ile
217                700                705                710
219  aat gat gct ttc cgt ctg aat gac aac agc cta gag ttt ctg ggg ata      2215
220  Asn Asp Ala Phe Arg Leu Asn Asp Asn Ser Leu Glu Phe Leu Gly Ile
221                715                720                725
223  cag cca aca ctt gga cct cct aac cag ccc cct gtt tcc ata tgg ctg      2263
224  Gln Pro Thr Leu Gly Pro Pro Asn Gln Pro Pro Val Ser Ile Trp Leu
225                730                735                740
227  att gtt ttt gga gtt gtg atg gga gtg ata gtg gtt ggc att gtc atc      2311
228  Ile Val Phe Gly Val Val Met Gly Val Ile Val Val Gly Ile Val Ile
229                745                750                755
231  ctg atc ttc act ggg atc aga gat cgg aag aag aaa aat aaa gca aga      2359
232  Leu Ile Phe Thr Gly Ile Arg Asp Arg Lys Lys Lys Asn Lys Ala Arg
233  760                765                770                775
235  agt gga gaa aat cct tat gcc tcc atc gat att agc aaa gga gaa aat      2407
236  Ser Gly Glu Asn Pro Tyr Ala Ser Ile Asp Ile Ser Lys Gly Glu Asn
237                780                785                790
239  aat cca gga ttc caa aac act gat gat gtt cag acc tcc ttt      2449
240  Asn Pro Gly Phe Gln Asn Thr Asp Asp Val Gln Thr Ser Phe
241                795                800                805
243  tagaaaaatc tatgtttttc ctcttgaggt gattttgttg tatgtaaatg ttaatttcac 2509
244  ggtatagaaa atataagatg ataaagatat cattaaatgt caaaactatg actctgttca 2569
245  gaaaaaaaaat tgtccaaaga caacatggcc aaggagagag catcttcatt gacattgctt 2629
246  tcagtatttta tttctgtctc tggatttgac ttctgttctg tttcttaata aggattttgt 2689
247  attagagtat attagggaaa gtgtgtattt ggtctcacag gctgttcagg gataatctaa 2749
248  atgtaaatgt ctgttgaatt tctgaagttg aaaacaagga tatatcattg gagcaagtgt 2809
249  tggatcttgt atggaatatg gatgatacac ttgtaaggac agtgcctggg aactggtgta 2869
250  gctgcaagga ttgagaatgg catgcattag ctcaactttca tttaatccat tgtcaaggat 2929
251  gacatgcttt cttcacagta actcagttca agtactatgg tgatttgcct acagtgatgt 2989
252  ttggaatcga tcatgctttc ttcaaggtga caggtctaaa gagagaagaa tccagggaac 3049
253  aggtagagga cattgctttt tcaacttccaa ggtgcttgat caacatctcc ctgacaacac 3109
254  aaaactagag ccaggggcct ccgtgaactc ccagagcatg cctgatagaa actcatttct 3169
255  actgttctct aactgtggag tgaatggaaa ttccaactgt atgttcaccc tctgaagtgg 3229
256  gtacccagtc tcttaaactc tttgtatttg ctcacagtgt ttgagcagtg ctgagcacia 3289
257  agcagacact caataaatgc tagattttaca cactccttgt gctta 3334
259 <210> SEQ ID NO: 2
260 <211> LENGTH: 805

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```

261 <212> TYPE: PRT
262 <213> ORGANISM: Homo sapiens
264 <400> SEQUENCE: 2
265 Met Ser Ser Ser Ser Trp Leu Leu Leu Ser Leu Val Ala Val Thr Ala
266 1 5 10 15
267 Ala Gln Ser Thr Ile Glu Glu Gln Ala Lys Thr Phe Leu Asp Lys Phe
268 20 25 30
269 Asn His Glu Ala Glu Asp Leu Phe Tyr Gln Ser Ser Leu Ala Ser Trp
270 35 40 45
271 Asn Tyr Asn Thr Asn Ile Thr Glu Glu Asn Val Gln Asn Met Asn Asn
272 50 55 60
273 Ala Gly Asp Lys Trp Ser Ala Phe Leu Lys Glu Gln Ser Thr Leu Ala
274 65 70 75 80
275 Gln Met Tyr Pro Leu Gln Glu Ile Gln Asn Leu Thr Val Lys Leu Gln
276 85 90 95
277 Leu Gln Ala Leu Gln Gln Asn Gly Ser Ser Val Leu Ser Glu Asp Lys
278 100 105 110
279 Ser Lys Arg Leu Asn Thr Ile Leu Asn Thr Met Ser Thr Ile Tyr Ser
280 115 120 125
281 Thr Gly Lys Val Cys Asn Pro Asp Asn Pro Gln Glu Cys Leu Leu Leu
282 130 135 140
283 Glu Pro Gly Leu Asn Glu Ile Met Ala Asn Ser Leu Asp Tyr Asn Glu
284 145 150 155 160
285 Arg Leu Trp Ala Trp Glu Ser Trp Arg Ser Glu Val Gly Lys Gln Leu
286 165 170 175
287 Arg Pro Leu Tyr Glu Glu Tyr Val Val Leu Lys Asn Glu Met Ala Arg
288 180 185 190
289 Ala Asn His Tyr Glu Asp Tyr Gly Asp Tyr Trp Arg Gly Asp Tyr Glu
290 195 200 205
291 Val Asn Gly Val Asp Gly Tyr Asp Tyr Ser Arg Gly Gln Leu Ile Glu
292 210 215 220
293 Asp Val Glu His Thr Phe Glu Glu Ile Lys Pro Leu Tyr Glu His Leu
294 225 230 235 240
295 His Ala Tyr Val Arg Ala Lys Leu Met Asn Ala Tyr Pro Ser Tyr Ile
296 245 250 255
297 Ser Pro Ile Gly Cys Leu Pro Ala His Leu Leu Gly Asp Met Trp Gly
298 260 265 270
299 Arg Phe Trp Thr Asn Leu Tyr Ser Leu Thr Val Pro Phe Gly Gln Lys
300 275 280 285
303 Pro Asn Ile Asp Val Thr Asp Ala Met Val Asp Gln Ala Trp Asp Ala
304 290 295 300
305 Gln Arg Ile Phe Lys Glu Ala Glu Lys Phe Phe Val Ser Val Gly Leu
306 305 310 315 320
307 Pro Asn Met Thr Gln Gly Phe Trp Glu Asn Ser Met Leu Thr Asp Pro
308 325 330 335
309 Gly Asn Val Gln Lys Ala Val Cys His Pro Thr Ala Trp Asp Leu Gly
310 340 345 350
311 Lys Gly Asp Phe Arg Ile Leu Met Cys Thr Lys Val Thr Met Asp Asp
312 355 360 365

```

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:384 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:388 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:389 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:390 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:391 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:392 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:393 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:394 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:395 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:396 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:397 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:399 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:403 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:404 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:408 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:409 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
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L:413 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:415 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:416 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
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L:420 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:421 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:422 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:423 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:424 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:792 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:793 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:794 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:795 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:796 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7

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L:797 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:799 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7